

SEQUENCE LISTING

<110> Max Planck Gesellschaft zur Förderung der Wissensc

<120> Substance binding human IgG Fc receptor IIb

<130> 30287P-EP

<140>

<141>

<160> 11

<170> PatentIn Ver. 2.1

<210> 1

<211> 172

<212> PRT

<213> Human

<400> 1

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Leu	Gln	Glu	Asp	Ser	Val	Thr	Leu	Thr	Cys	Gln	Gly	Ala	Arg	Ser	Pro
			20					25					30		

Glu	Ser	Asp	Ser	Ile	Gln	Trp	Phe	His	Asn	Gly	Asn	Leu	Ile	Pro	Thr
		35					40					45			

His	Thr	Gln	Pro	Ser	Tyr	Arg	Phe	Lys	Ala	Asn	Asn	Asn	Asp	Ser	Gly
	50					55					60				

Glu	Tyr	Thr	Cys	Gln	Thr	Gly	Gln	Thr	Ser	Leu	Ser	Asp	Pro	Val	His
65					70					75					80

Leu	Thr	Val	Leu	Ser	Glu	Trp	Leu	Val	Leu	Gln	Thr	Pro	His	Leu	Glu
			85						90					95	

Phe	Gln	Glu	Gly	Glu	Thr	Ile	Met	Leu	Arg	Cys	His	Ser	Trp	Lys	Asp
		100						105					110		

Lys	Pro	Leu	Val	Lys	Val	Thr	Phe	Phe	Gln	Asn	Gly	Lys	Ser	Gln	Lys
		115					120					125			

Phe	Ser	Arg	Leu	Asp	Pro	Thr	Phe	Ser	Ile	Pro	Gln	Ala	Asn	His	Ser
	130					135					140				

His	Ser	Gly	Asp	Tyr	His	Cys	Thr	Gly	Asn	Ile	Gly	Tyr	Thr	Leu	Phe
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Ser	Ser	Lys	Pro	Val	Thr	Ile	Thr	Val	Gln	Val	Pro
			165						170		

<210> 2

<211> 172

<212> PRT

<213> Human

<400> 2

Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Gln Trp Ile Asn Val

<210>	3
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<213>	Human

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Ser Lys Lys Phe Ser Arg Ser Asp Pro Asn Phe Ser Gly
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<210> 4
<211> 312
<212> DNA
<213> hybridoma
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<220>  
<221> CDS  
<222> (1) .. (312)
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Arg Ile Gln Leu Thr 5 Gln Ser Pro Ser Ser 10 Leu Ser Ala Ser Leu Gly 15
gaa aga gtc agt ctc act tgt cgg gca agt cag gaa att agt ggt tac 96
Glu Arg Val Ser Leu Thr Cys Arg Ala Ser 25 Gln Glu Ile 30 Ser Gly Tyr

3/7

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tta agc tgg ctt cag cag aaa cca gat gga act att aaa cgc ctg atc   144
Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile Lys Arg Leu Ile
      35                      40                      45

tac gcc aca tcc gct tta gat tct ggt gtc cca aaa agg ttc agt ggc   192
Tyr Ala Thr Ser Ala Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
      50                      55                      60

agt ggg tct ggg tca aat tat tct ctc acc atc agc agc ctt gag tct   240
Ser Gly Ser Gly Ser Asn Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
      65                      70                      75                      80

gaa gat ttt gca gac tat tac tgt cta caa tat gct aat tat ccg tac   288
Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ala Asn Tyr Pro Tyr
      85                      90                      95

acg ttc gga ggg ggg acc aag ctg   312
Thr Phe Gly Gly Gly Thr Lys Leu
      100

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<210> 5
 <211> 104
 <212> PRT
 <213> hybridoma

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<400> 5
Arg Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
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Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr
      20                      25                      30

Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile Lys Arg Leu Ile
      35                      40                      45

Tyr Ala Thr Ser Ala Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
      50                      55                      60

Ser Gly Ser Gly Ser Asn Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
      65                      70                      75                      80

Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ala Asn Tyr Pro Tyr
      85                      90                      95

Thr Phe Gly Gly Gly Thr Lys Leu
      100

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<210> 6
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 <212> DNA
 <213> hybridoma

<220>
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 <222> (1)..(312)

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<400> 6
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  1                      5                      10                      15

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gtg aag att tcc tgc aag gct tct ggc tac acc ttc act gac tac tat 96
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr
      20      25      30

ata tac tgg gtg aaa cag tgg cct gga cag gga ctt gag tgg att gga 144
Ile Tyr Trp Val Lys Gln Trp Pro Gly Gln Gly Leu Glu Trp Ile Gly
      35      40      45

tgg att ttt cct gga act ggt aat act tac tac aat gaa aac ttc aag 192
Trp Ile Phe Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys
      50      55      60

gac aag gcc aca ctt act ata gat aga tcc tcc agc aca gcc tac atg 240
Asp Lys Ala Thr Leu Thr Ile Asp Arg Ser Ser Ser Thr Ala Tyr Met
      65      70      75      80

ttg ctc ggc agc ctg acc tct gag gac tct gcg gtc tat ttc tgt tat 288
Leu Leu Gly Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Tyr
      85      90      95

ggt ccg ttt gct tac tgg ggc caa 312
Gly Pro Phe Ala Tyr Trp Gly Gln
      100

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<210> 7
 <211> 104
 <212> PRT
 <213> hybridoma

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      20      25      30

Ile Tyr Trp Val Lys Gln Trp Pro Gly Gln Gly Leu Glu Trp Ile Gly
      35      40      45

Trp Ile Phe Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys
      50      55      60

Asp Lys Ala Thr Leu Thr Ile Asp Arg Ser Ser Ser Thr Ala Tyr Met
      65      70      75      80

Leu Leu Gly Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Tyr
      85      90      95

Gly Pro Phe Ala Tyr Trp Gly Gln
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<210> 8
 <211> 331
 <212> DNA
 <213> hybridoma

<220>
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 <222> (1)..(330)

<400> 8

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Arg Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

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```

cag agg gcc acc atc tca tac agg gcc agc aaa agt gtc agt aca tct 96
Gln Arg Ala Thr Ile Ser Tyr Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30

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ggc tat agt tat atg cac tgg aac caa cag aaa cca gga cag cca ccc 144
Gly Tyr Ser Tyr Met His Trp Asn Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

```

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aga ctc ctc atc tat ctt gta tcc aac cta gaa tct ggg gtc cct gcc 192
Arg Leu Leu Ile Tyr Leu Val Ser Asn Leu Glu Ser Gly Val Pro Ala
50 55 60

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agg ttc agt ggc agt ggg tct ggg aca gac ttc acc ctc aac atc cat 240
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

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cct gtg gag gag gag gat gct gca acc tat tac tgt cag cac att agg 288
Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ile Arg
85 90 95

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gag ctt aca cgt tcg gag ggg gga cca agc tgg aga tct aac a 331
Glu Leu Thr Arg Ser Glu Gly Gly Pro Ser Trp Arg Ser Asn
100 105 110

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<210> 9

<211> 110

<212> PRT

<213> hybridoma

<400> 9

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Arg Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

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Gln Arg Ala Thr Ile Ser Tyr Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30

```

```

Gly Tyr Ser Tyr Met His Trp Asn Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

```

```

Arg Leu Leu Ile Tyr Leu Val Ser Asn Leu Glu Ser Gly Val Pro Ala
50 55 60

```

```

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

```

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Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ile Arg
85 90 95

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Glu Leu Thr Arg Ser Glu Gly Gly Pro Ser Trp Arg Ser Asn
100 105 110

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<210> 10

<211> 343

<212> DNA

<213> hybridoma

<220>

<221> CDS

<222> (1)..(342)

<400> 10

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Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser
1 5 10 15

ctg tcc atc aca tgc acc gtc tca ggg ttc tca tta act agc tat ggt 96
Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr Gly
20 25 30

gta cac tgg gtt cgc cag cct cca gga aag ggt ctg gag tgg ctg gta 144
Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Val
35 40 45

gtg ata tgg agt gat gga agc aca acc tat aat tca gct ctc aaa tcc 192
Val Ile Trp Ser Asp Gly Ser Thr Thr Tyr Asn Ser Ala Leu Lys Ser
50 55 60

aga ctg agc atc agc aag gac aac tcc aag agc caa gtt ttc tta aaa 240
Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys
65 70 75 80

atg aac agt ctc caa act gat gac aca gcc atg tac tac tgt gcc aga 288
Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg
85 90 95

gag cct ccc acg acg tac gtt tgc tta ctg ggg cca agg gac cac tct 336
Glu Pro Pro Thr Thr Tyr Val Cys Leu Leu Gly Pro Arg Asp His Ser
100 105 110

aga tta a 343
Arg Leu

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<210> 11

<211> 114

<212> PRT

<213> hybridoma

<400> 11

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Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser
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Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr Gly
20 25 30

Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Val
35 40 45

Val Ile Trp Ser Asp Gly Ser Thr Thr Tyr Asn Ser Ala Leu Lys Ser
50 55 60

Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys
65 70 75 80

Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg
85 90 95

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Glu Pro Pro Thr Thr Tyr Val Cys Leu Leu Gly Pro Arg Asp His Ser
100 105 110

Arg Leu

SEQUENCE LISTING

<110> Max Planck Gesellschaft zur Förderung der Wissensc

<120> Substance binding human IgG Fc receptor IIb (Fc gamma
RIIb)

<130> 30287P_WO HC

<140> PCT/EP2004/013450

<141> 2004-11-26

<150> EP03027000.3

<151> 2003-11-26

<160> 11

<170> PatentIn Ver: 2.1

<210> 1

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<212> PRT

<213> human

<220>

<223> Fc gamma RIIa

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Leu	Gln	Glu	Asp	Ser	Val	Thr	Leu	Thr	Cys	Gln	Gly	Ala	Arg	Ser	Pro
			20					25					30		

Glu	Ser	Asp	Ser	Ile	Gln	Trp	Phe	His	Asn	Gly	Asn	Leu	Ile	Pro	Thr
		35					40					45			

His	Thr	Gln	Pro	Ser	Tyr	Arg	Phe	Lys	Ala	Asn	Asn	Asn	Asp	Ser	Gly
	50					55					60				

Glu	Tyr	Thr	Cys	Gln	Thr	Gly	Gln	Thr	Ser	Leu	Ser	Asp	Pro	Val	His
65					70					75					80

Leu	Thr	Val	Leu	Ser	Glu	Trp	Leu	Val	Leu	Gln	Thr	Pro	His	Leu	Glu
				85					90					95	

Phe	Gln	Glu	Gly	Glu	Thr	Ile	Met	Leu	Arg	Cys	His	Ser	Trp	Lys	Asp
			100					105					110		

Lys	Pro	Leu	Val	Lys	Val	Thr	Phe	Phe	Gln	Asn	Gly	Lys	Ser	Gln	Lys
		115					120					125			

Phe	Ser	Arg	Leu	Asp	Pro	Thr	Phe	Ser	Ile	Pro	Gln	Ala	Asn	His	Ser
	130					135					140				

His	Ser	Gly	Asp	Tyr	His	Cys	Thr	Gly	Asn	Ile	Gly	Tyr	Thr	Leu	Phe
145					150					155					160

Ser Ser Lys Pro Val Thr Ile Thr Val Gln Val Pro
165 170

<210> 2
<211> 172
<212> PRT
<213> human

<220>
<223> Fc gamma RIIB

<400> 2
Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Gln Trp Ile Asn Val
1 5 10 15
Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Arg Gly Thr His Ser Pro
20 25 30
Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr
35 40 45
His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly
50 55 60
Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His
65 70 75 80
Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu
85 90 95
Phe Gln Glu Gly Glu Thr Ile Val Leu Arg Cys His Ser Trp Lys Asp
100 105 110
Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Lys Lys
115 120 125
Phe Ser Arg Ser Asp Pro Asn Phe Ser Ile Pro Gln Ala Asn His Ser
130 135 140
His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Tyr
145 150 155 160
Ser Ser Lys Pro Val Thr Ile Thr Val Gln Ala Pro
165 170

<210> 3
<211> 13
<212> PRT
<213> human

<220>
<223> glycopeptide CDE [126-137]

Ser Lys Lys Phe Ser Arg Ser Asp Pro Asn Phe Ser Gly
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25659588.1

<400> 5

Arg Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr
20 25 30

Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile Lys Arg Leu Ile
35 40 45

Tyr Ala Thr Ser Ala Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Ser Asn Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
65 70 75 80

Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ala Asn Tyr Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu
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<210> 6

<211> 312

<212> DNA

<213> Unknown Organism

<220>

<221> CDS

<222> (1)..(312)

<223> variable heavy region of mAb GB3

<220>

<223> Description of Unknown Organism: sequence
comprised by an antibody

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Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser
1 5 10 15

gtg aag att tcc tgc aag gct tct ggc tac acc ttc act gac tac tat 96
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr
20 25 30

ata tac tgg gtg aaa cag tgg cct gga cag gga ctt gag tgg att gga 144
Ile Tyr Trp Val Lys Gln Trp Pro Gly Gln Gly Leu Glu Trp Ile Gly
35 40 45

tgg att ttt cct gga act ggt aat act tac tac aat gaa aac ttc aag 192
Trp Ile Phe Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys
50 55 60

gac aag gcc aca ctt act ata gat aga tcc tcc agc aca gcc tac atg 240

Asp	Lys	Ala	Thr	Leu	Thr	Ile	Asp	Arg	Ser	Ser	Ser	Thr	Ala	Tyr	Met	
65					70					75					80	
ttg	ctc	ggc	agc	ctg	acc	tct	gag	gac	tct	gcg	gtc	tat	ttc	tgt	tat	288
Leu	Leu	Gly	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys	Tyr	
				85					90					95		
ggc	ccg	ttt	gct	tac	tgg	ggc	caa									312
Gly	Pro	Phe	Ala	Tyr	Trp	Gly	Gln									
				100												

<210> 7
 <211> 104
 <212> PRT
 <213> Unknown Organism
 <223> Description of Unknown Organism: sequence
 comprised by an antibody

Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Lys	Pro	Gly	Ala	Ser	
1				5					10					15		
Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	Tyr	Tyr	
			20					25					30			
Ile	Tyr	Trp	Val	Lys	Gln	Trp	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	
		35					40					45				
Trp	Ile	Phe	Pro	Gly	Thr	Gly	Asn	Thr	Tyr	Tyr	Asn	Glu	Asn	Phe	Lys	
	50					55					60					
Asp	Lys	Ala	Thr	Leu	Thr	Ile	Asp	Arg	Ser	Ser	Ser	Thr	Ala	Tyr	Met	
65					70					75					80	
Leu	Leu	Gly	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys	Tyr	
				85					90					95		
Gly	Pro	Phe	Ala	Tyr	Trp	Gly	Gln									
				100												

<210> 8
 <211> 309
 <212> DNA
 <213> Unknown Organism

 <220>
 <221> CDS
 <222> (1)..(309)
 <223> variable light region of mAb CE5

 <220>
 <223> Description of Unknown Organism: sequence
 comprised by an antibody

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<400> 8
gag ctc acc cag tct cca gcc tcc ctt tct gcg tct gtg gga gaa act 48
Glu Leu Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly Glu Thr
  1             5             10             15

gtc acc atc aca tgt cga gca agt ggg aat att cac aat tat tta gca 96
Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala
          20             25             30

tgg tat cag cag aaa cag gga aaa tct cct cag ctc ctg gtc tat tat 144
Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val Tyr Tyr
          35             40             45

aca aca acc tta gca gat ggt gtg cca tca agg ttc agt ggc agt gga 192
Thr Thr Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
          50             55             60

tca gga aca caa tat tct ctc aag atc aac agc ctg caa cct gaa gat 240
Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Pro Glu Asp
          65             70             75             80

ttt ggg agt tat tac tgt caa cat ttt tgg agt act cct cgg acg ttc 288
Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Arg Thr Phe
          85             90             95

ggt gga ggg acc aag ctc gag 309
Gly Gly Gly Thr Lys Leu Glu
          100

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<210> 9
<211> 103
<212> PRT
<213> Unknown Organism
<223> Description of Unknown Organism: sequence
        comprised by an antibody

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Glu Leu Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly Glu Thr
  1             5             10             15

Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala
          20             25             30

Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val Tyr Tyr
          35             40             45

Thr Thr Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
          50             55             60

Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Pro Glu Asp
          65             70             75             80

Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Arg Thr Phe
          85             90             95

Gly Gly Gly Thr Lys Leu Glu

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<210> 10
 <211> 339
 <212> DNA
 <213> Unknown Organism

<220>
 <221> CDS
 <222> (3)..(338)
 <223> variable heavy region of mAb CE5

<220>
 <223> Description of Unknown Organism: sequence
 comprised by an antibody

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 Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
 1 5 10 15
 atc aca tgc acc gtc tca ggg ttc tca tta acc ggc tat ggt gta aac 95
 Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr Gly Val Asn
 20 25 30
 tgg gtt cgc cag cct cca gga aag ggt ctg gag tgg ctg gga atg att 143
 Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Met Ile
 35 40 45
 tgg ggt gat gga aac aca gac tat aat tca gct ctc aaa tcc aga ctg 191
 Trp Gly Asp Gly Asn Thr Asp Tyr Asn Ser Ala Leu Lys Ser Arg Leu
 50 55 60
 agc atc agc aag gac aac tcc aag agc caa gtt ttc tta aaa atg aac 239
 Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
 65 70 75
 agt ctg cac act gat gac aca gcc agg tac tac tgt gcc aga gag aga 287
 Ser Leu His Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala Arg Glu Arg
 80 85 90 95
 gat tat agg ctt gac tac tgg ggc caa ggg acc acg gtc acc gtc tcc 335
 Asp Tyr Arg Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 100 105 110
 tca g 339
 Ser

<210> 11
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 <212> PRT
 <213> Unknown Organism
 <223> Description of Unknown Organism: sequence
 comprised by an antibody

<400> 11

Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Ile
1 5 10 15

Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr Gly Val Asn Trp
20 25 30

Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Met Ile Trp
35 40 45

Gly Asp Gly Asn Thr Asp Tyr Asn Ser Ala Leu Lys Ser Arg Leu Ser
50 55 60

Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn Ser
65 70 75 80

Leu His Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala Arg Glu Arg Asp
85 90 95

Tyr Arg Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
100 105 110

30287PW1.txt
SEQUENCE LISTING

<110> Max Planck Gesellschaft zur Förderung der Wissenc

<120> Substance binding human IgG Fc receptor IIb (Fc gamma
RIIb)

<130> 30287P_WO HC

<140> PCT/EP2004/013450

<141> 2004-11-26

<150> EP03027000.3

<151> 2003-11-26

<160> 11

<170> PatentIn Ver. 2.1

<210> 1

<211> 172

<212> PRT

<213> human

<220>

<223> Fc gamma RIIa

<400> 1

Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Pro Trp Ile Asn Val
1 5 10 15Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Gln Gly Ala Arg Ser Pro
20 25 30Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr
35 40 45His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly
50 55 60Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His
65 70 75 80Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu
85 90 95Phe Gln Glu Gly Glu Thr Ile Met Leu Arg Cys His Ser Trp Lys Asp
100 105 110Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Gln Lys
115 120 125Phe Ser Arg Leu Asp Pro Thr Phe Ser Ile Pro Gln Ala Asn His Ser
130 135 140His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe
145 150 155 160Ser Ser Lys Pro Val Thr Ile Thr Val Gln Val Pro
165 170

<210> 2
 <211> 172
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 <213> human

<220>
 <223> Fc gamma RIIB

<400> 2

Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Gln Trp Ile Asn Val
 1 5 10 15
 Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Arg Gly Thr His Ser Pro
 20 25 30
 Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr
 35 40 45
 His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly
 50 55 60
 Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His
 65 70 75 80
 Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu
 85 90 95
 Phe Gln Glu Gly Glu Thr Ile Val Leu Arg Cys His Ser Trp Lys Asp
 100 105 110
 Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Lys Lys
 115 120 125
 Phe Ser Arg Ser Asp Pro Asn Phe Ser Ile Pro Gln Ala Asn His Ser
 130 135 140
 His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Tyr
 145 150 155 160
 Ser Ser Lys Pro Val Thr Ile Thr Val Gln Ala Pro
 165 170

<210> 3
 <211> 13
 <212> PRT
 <213> human

<220>
 <223> glycopeptide CDE [126-137]

<400> 3

Ser Lys Lys Phe Ser Arg Ser Asp Pro Asn Phe Ser Gly
 1 5 10

<210> 4
 <211> 312
 <212> DNA
 <213> Unknown Organism

<220>

<221> CDS

<222> (1)..(312)

<223> variable light region of mAb GB3

<220>

<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 4

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aga att cag ctg acc cag tct cca tcc tcc tta tct gcc tct ctg gga 48
Arg Ile Gln Leu Thr 5 Gln Ser Pro Ser Ser 10 Leu Ser Ala Ser Leu Gly 15

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gaa aga gtc agt ctc act tgt cgg gca agt cag gaa att agt ggt tac 96
Glu Arg Val Ser 20 Leu Thr Cys Arg Ala 25 Ser Gln Glu Ile Ser 30 Gly Tyr

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tta agc tgg ctt cag cag aaa cca gat gga act att aaa cgc ctg atc 144
Leu Ser Trp 35 Leu Gln Gln Lys Pro 40 Asp Gly Thr Ile Lys 45 Arg Leu Ile

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tac gcc aca tcc gct tta gat tct ggt gtc cca aaa agg ttc agt ggc 192
Tyr Ala 50 Thr Ser Ala Leu Asp 55 Ser Gly Val Pro Lys 60 Arg Phe Ser Gly

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agt ggg tct ggg tca aat tat tct ctc acc atc agc agc ctt gag tct 240
Ser Gly Ser Gly Ser Asn 70 Tyr Ser Leu Thr Ile 75 Ser Ser Leu Glu Ser 80

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gaa gat ttt gca gac tat tac tgt cta caa tat gct aat tat ccg tac 288
Glu Asp Phe Ala Asp 85 Tyr Tyr Cys Leu Gln 90 Tyr Ala Asn Tyr Pro 95 Tyr

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acg ttc gga ggg ggg acc aag ctg 312
Thr Phe Gly 100 Gly Gly Thr Lys Leu

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<210> 5

<211> 104

<212> PRT

<213> Unknown Organism

<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 5

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Arg Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

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Glu Arg Val Ser 20 Leu Thr Cys Arg Ala 25 Ser Gln Glu Ile Ser 30 Gly Tyr

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Leu Ser Trp 35 Leu Gln Gln Lys Pro 40 Asp Gly Thr Ile Lys 45 Arg Leu Ile

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Tyr Ala 50 Thr Ser Ala Leu Asp 55 Ser Gly Val Pro Lys 60 Arg Phe Ser Gly

```

```

Ser Gly Ser Gly Ser Asn 70 Tyr Ser Leu Thr Ile 75 Ser Ser Leu Glu Ser 80

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Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ala Asn Tyr Pro Tyr

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Thr Phe Gly Gly Gly Thr Lys Leu
100

<210> 6
<211> 312
<212> DNA
<213> Unknown Organism

<220>
<221> CDS
<222> (1)..(312)
<223> variable heavy region of mAb GB3

<220>
<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 6
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Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser
1 5 10 15
gtg aag att tcc tgc aag gct tct ggc tac acc ttc act gac tac tat 96
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr
20 25 30
ata tac tgg gtg aaa cag tgg cct gga cag gga ctt gag tgg att gga 144
Ile Tyr Trp Val Lys Gln Trp Pro Gly Gln Gly Leu Glu Trp Ile Gly
35 40 45
tgg att ttt cct gga act ggt aat act tac tac aat gaa aac ttc aag 192
Trp Ile Phe Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys
50 55 60
gac aag gcc aca ctt act ata gat aga tcc tcc agc aca gcc tac atg 240
Asp Lys Ala Thr Leu Thr Ile Asp Arg Ser Ser Ser Thr Ala Tyr Met
65 70 75 80
ttg ctc ggc agc ctg acc tct gag gac tct gcg gtc tat ttc tgt tat 288
Leu Leu Gly Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Tyr
85 90 95
ggt ccg ttt gct tac tgg ggc caa 312
Gly Pro Phe Ala Tyr Trp Gly Gln
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<210> 7
<211> 104
<212> PRT
<213> Unknown Organism
<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 7
val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser
1 5 10 15

val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr
Page 4

20 25 30
 Ile Tyr Trp Val Lys Gln Trp Pro Gly Gln Gly Leu Glu Trp Ile Gly
 35 40 45
 Trp Ile Phe Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys
 50 55 60
 Asp Lys Ala Thr Leu Thr Ile Asp Arg Ser Ser Ser Thr Ala Tyr Met
 65 70 75 80
 Leu Leu Gly Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Tyr
 85 90 95
 Gly Pro Phe Ala Tyr Trp Gly Gln
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<210> 8

<211> 309

<212> DNA

<213> Unknown Organism

<220>

<221> CDS

<222> (1)..(309)

<223> variable light region of mAb CE5

<220>

<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 8

gag ctc acc cag tct cca gcc tcc ctt tct gcg tct gtg gga gaa act 48
 Glu Leu Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly Glu Thr
 1 5 10 15

gtc acc atc aca tgt cga gca agt ggg aat att cac aat tat tta gca 96
 Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala
 20 25 30

tgg tat cag cag aaa cag gga aaa tct cct cag ctc ctg gtc tat tat 144
 Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val Tyr Tyr
 35 40 45

aca aca acc tta gca gat ggt gtg cca tca agg ttc agt ggc agt gga 192
 Thr Thr Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60

tca gga aca caa tat tct ctc aag atc aac agc ctg caa cct gaa gat 240
 Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Pro Glu Asp
 65 70 75 80

ttt ggg agt tat tac tgt caa cat ttt tgg agt act cct cgg acg ttc 288
 Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Arg Thr Phe
 85 90 95

ggt gga ggg acc aag ctc gag 309
 Gly Gly Gly Thr Lys Leu Glu
 100

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<210> 9
<211> 103
<212> PRT
<213> Unknown Organism
<223> Description of Unknown Organism: sequence
      comprised by an antibody

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<400> 9
Glu Leu Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly Glu Thr
1 5 10 15
Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala
20 25 30
Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val Tyr Tyr
35 40 45
Thr Thr Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60
Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Pro Glu Asp
65 70 75 80
Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Arg Thr Phe
85 90 95
Gly Gly Gly Thr Lys Leu Glu
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<210> 10
<211> 339
<212> DNA
<213> Unknown Organism
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<220>  
<221> CDS  
<222> (3)..(338)  
<223> variable heavy region of mAb CE5
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<220>
<223> Description of Unknown Organism: sequence
      comprised by an antibody
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30287PW1.txt

Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
65 70 75
agt ctg cac act gat gac aca gcc agg tac tac tgt gcc aga gag aga 287
Ser Leu His Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala Arg Glu Arg 95
80 85 90
gat tat agg ctt gac tac tgg ggc caa ggg acc acg gtc acc gtc tcc 335
Asp Tyr Arg Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser 110
100 105 110
tca g 339
Ser

<210> 11
<211> 112
<212> PRT
<213> Unknown Organism
<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 11
Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Ile
1 5 10 15
Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr Gly Val Asn Trp
20 25 30
Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Met Ile Trp
35 40 45
Gly Asp Gly Asn Thr Asp Tyr Asn Ser Ala Leu Lys Ser Arg Leu Ser
50 55 60
Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn Ser
65 70 75 80
Leu His Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala Arg Glu Arg Asp
85 90 95
Tyr Arg Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
100 105 110

SEQUENCE LISTING

<110> Max Planck Gesellschaft zur Förderung der Wissensc

<120> Substance binding human IgG Fc receptor IIb (Fc gamma
 RIIb)

<130> 30287P_WO HC

<140> PCT/EP2004/013450

<141> 2004-11-26

<150> EP03027000.3

<151> 2003-11-26

<160> 11

<170> PatentIn Ver. 2.1

<210> 1

<211> 172

<212> PRT

<213> human

<220>

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<400> 1

Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Pro Trp Ile Asn Val
 1 5 10 15

Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Gln Gly Ala Arg Ser Pro
 20 25 30

Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr
 35 40 45

His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly
 50 55 60

Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His
 65 70 75 80

Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu
 85 90 95

Phe Gln Glu Gly Glu Thr Ile Met Leu Arg Cys His Ser Trp Lys Asp
 100 105 110

Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Gln Lys
 115 120 125

Phe Ser Arg Leu Asp Pro Thr Phe Ser Ile Pro Gln Ala Asn His Ser
 130 135 140

His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe
 145 150 155 160

Ser Ser Lys Pro Val Thr Ile Thr Val Gln Val Pro
 165 170

<210> 2
 <211> 172
 <212> PRT
 <213> human

<220>
 <223> Fc gamma RIIb

<400> 2
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 1 5 10 15

Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Arg Gly Thr His Ser Pro
 20 25 30

Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr
 35 40 45

His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly
 50 55 60

Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His
 65 70 75 80

Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu
 85 90 95

Phe Gln Glu Gly Glu Thr Ile Val Leu Arg Cys His Ser Trp Lys Asp
 100 105 110

Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Lys Lys
 115 120 125

Phe Ser Arg Ser Asp Pro Asn Phe Ser Ile Pro Gln Ala Asn His Ser
 130 135 140

His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Tyr
 145 150 155 160

Ser Ser Lys Pro Val Thr Ile Thr Val Gln Ala Pro
 165 170

<210> 3
 <211> 13
 <212> PRT
 <213> human

<220>
 <223> glycopeptide CDE [126-137]

<400> 3
 Ser Lys Lys Phe Ser Arg Ser Asp Pro Asn Phe Ser Gly
 1 5 10

<210> 4
 <211> 312
 <212> DNA
 <213> Unknown Organism

<220>
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 <222> (1)..(312)
 <223> variable light region of mAb GB3

<220>
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 comprised by an antibody

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 1 5 10 15
 gaa aga gtc agt ctc act tgt cgg gca agt cag gaa att agt ggt tac 96
 Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr
 20 25 30

tta agc tgg ctt cag cag aaa cca gat gga act att aaa cgc ctg atc 144
 Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile Lys Arg Leu Ile
 35 40 45

tac gcc aca tcc gct tta gat tct ggt gtc cca aaa agg ttc agt ggc 192
 Tyr Ala Thr Ser Ala Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
 50 55 60

agt ggg tct ggg tca aat tat tct ctc acc atc agc agc ctt gag tct 240
 Ser Gly Ser Gly Ser Asn Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
 65 70 75 80

gaa gat ttt gca gac tat tac tgt cta caa tat gct aat tat ccg tac 288
 Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ala Asn Tyr Pro Tyr
 85 90 95

acg ttc gga ggg ggg acc aag ctg 312
 Thr Phe Gly Gly Gly Thr Lys Leu
 100

<210> 5
 <211> 104
 <212> PRT
 <213> Unknown Organism
 <223> Description of Unknown Organism: sequence
 comprised by an antibody

<400> 5
 Arg Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15

Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr
 20 25 30

Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile Lys Arg Leu Ile
 35 40 45

Tyr Ala Thr Ser Ala Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Ser Asn Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
 65 70 75 80

Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ala Asn Tyr Pro Tyr
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu

<210> 6
 <211> 312
 <212> DNA
 <213> Unknown Organism

<220>
 <221> CDS
 <222> (1)..(312)
 <223> variable heavy region of mAb GB3

<220>
 <223> Description of Unknown Organism: sequence
 comprised by an antibody

<400> 6
 gtg cag ctg cag cag tct gga cct gag ctg gtg aag cct ggg gct tca 48
 Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser
 1 5 10 15
 gtg aag att tcc tgc aag gct tct ggc tac acc ttc act gac tac tat 96
 Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr
 20 25 30
 ata tac tgg gtg aaa cag tgg cct gga cag gga ctt gag tgg att gga 144
 Ile Tyr Trp Val Lys Gln Trp Pro Gly Gln Gly Leu Glu Trp Ile Gly
 35 40 45
 tgg att ttt cct gga act ggt aat act tac tac aat gaa aac ttc aag 192
 Trp Ile Phe Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys
 50 55 60
 gac aag gcc aca ctt act ata gat aga tcc tcc agc aca gcc tac atg 240
 Asp Lys Ala Thr Leu Thr Ile Asp Arg Ser Ser Ser Thr Ala Tyr Met
 65 70 75 80
 ttg ctc ggc agc ctg acc tct gag gac tct gcg gtc tat ttc tgt tat 288
 Leu Leu Gly Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Tyr
 85 90 95
 ggt ccg ttt gct tac tgg ggc caa 312
 Gly Pro Phe Ala Tyr Trp Gly Gln
 100

<210> 7
 <211> 104
 <212> PRT
 <213> Unknown Organism
 <223> Description of Unknown Organism: sequence
 comprised by an antibody

<400> 7
 Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser
 1 5 10 15
 Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr
 20 25 30
 Ile Tyr Trp Val Lys Gln Trp Pro Gly Gln Gly Leu Glu Trp Ile Gly
 35 40 45
 Trp Ile Phe Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys
 50 55 60
 Asp Lys Ala Thr Leu Thr Ile Asp Arg Ser Ser Ser Thr Ala Tyr Met
 65 70 75 80
 Leu Leu Gly Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Tyr
 85 90 95
 Gly Pro Phe Ala Tyr Trp Gly Gln
 100

<210> 8
 <211> 309
 <212> DNA
 <213> Unknown Organism

<220>
 <221> CDS
 <222> (1)..(309)
 <223> variable light region of mAb CE5

<220>
 <223> Description of Unknown Organism: sequence
 comprised by an antibody

<400> 8
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 Glu Leu Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly Glu Thr

1	5	10	15	
gtc acc atc aca tgt cga gca agt ggg aat att cac aat tat tta gca				96
Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala				
20		25	30	
tgg tat cag cag aaa cag gga aaa tct cct cag ctc ctg gtc tat tat				144
Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val Tyr Tyr				
35		40	45	
aca aca acc tta gca gat ggt gtg cca tca agg ttc agt ggc agt gga				192
Thr Thr Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly				
50		55	60	
tca gga aca caa tat tct ctc aag atc aac agc ctg caa cct gaa gat				240
Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Pro Glu Asp				
65		70	75	80
ttt ggg agt tat tac tgt caa cat ttt tgg agt act cct cgg acg ttc				288
Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Arg Thr Phe				
85		90	95	
ggg gga ggg acc aag ctc gag				309
Gly Gly Gly Thr Lys Leu Glu				
100				

<210> 9
 <211> 103
 <212> PRT
 <213> Unknown Organism
 <223> Description of Unknown Organism: sequence
 comprised by an antibody

<400> 9
 Glu Leu Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly Glu Thr
 1 5 10 15
 Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala
 20 25 30
 Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val Tyr Tyr
 35 40 45
 Thr Thr Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60
 Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Pro Glu Asp

65	70	75	80
Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Arg Thr Phe			
85	90	95	
Gly Gly Gly Thr Lys Leu Glu			
100			

<210> 10
 <211> 339
 <212> DNA
 <213> Unknown Organism

<220>
 <221> CDS
 <222> (3)..(338)
 <223> variable heavy region of mAb CE5

<220>
 <223> Description of Unknown Organism: sequence
 comprised by an antibody

<400> 10

tg cag gag tca gga cct ggc ctg gtg gcg ccc tca cag agc ctg tcc	47
Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser	
1 5 10 15	
atc aca tgc acc gtc tca ggg ttc tca tta acc ggc tat ggt gta aac	95
Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr Gly Val Asn	
20 25 30	
tgg gtt cgc cag cct cca gga aag ggt ctg gag tgg ctg gga atg att	143
Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Met Ile	
35 40 45	
tgg ggt gat gga aac aca gac tat aat tca gct ctc aaa tcc aga ctg	191
Trp Gly Asp Gly Asn Thr Asp Tyr Asn Ser Ala Leu Lys Ser Arg Leu	
50 55 60	
agc atc agc aag gac aac tcc aag agc caa gtt ttc tta aaa atg aac	239
Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn	
65 70 75	
agt ctg cac act gat gac aca gcc agg tac tac tgt gcc aga gag aga	287
Ser Leu His Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala Arg Glu Arg	
80 85 90 95	

gat tat agg ctt gac tac tgg ggc caa ggg acc acg gtc acc gtc tcc 335
 Asp Tyr Arg Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 100 105 110

tca g 339
 Ser

<210> 11

<211> 112

<212> PRT

<213> Unknown Organism

<223> Description of Unknown Organism: sequence
 comprised by an antibody

<400> 11

Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Ile
 1 5 10 15

Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr Gly Val Asn Trp
 20 25 30

Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Met Ile Trp
 35 40 45

Gly Asp Gly Asn Thr Asp Tyr Asn Ser Ala Leu Lys Ser Arg Leu Ser
 50 55 60

Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn Ser
 65 70 75 80

Leu His Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala Arg Glu Arg Asp
 85 90 95

Tyr Arg Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 100 105 110